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A new species of the genus *Odorrana* (Amphibia, Anura, Ranidae) from Guizhou Province, China

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Abstract

Based on morphological comparisons and molecular phylogenetics, a new species of the genus *Odorrana* from Xiuwen and Jinsha counties, Guizhou Province, China, is described. Phylogenetic analyses of mitochondrial 16S rRNA and COI gene sequences supported the new species as a sister species to *O. lipuensis*. The uncorrected p-distances of 16S rRNA and COI genes between the new species and its closest congeners were 2.6% and 4.4%, respectively. The new species is distinguished from its congeners by a combination of the following characters: (1) medium body size (SVL 37.0–39.0 mm in males and 49.4–52.2 mm in females); (2) tympanum distinctly visible, greater than one-half the diameter of the eye; (3) dorsolateral folds absent in males; (4) relative finger lengths: I < II < IV < III; (5) tibiotarsal articulation reaching the nostril when the leg is stretched forward; (6) bands on the dorsal surface of the hindlimb clear; and (7) vocal sacs absent in males.

Key Words

molecular phylogenetic analysis, morphology, new species, *Odorrana*

Introduction

Karst landforms, as unique global ecosystems, have become hotspots for biodiversity formation and differentiation due to their complex cave networks, isolated microhabitats, and stable microclimates (Clements et al. 2006; Grismer et al. 2021). In southern China, karst regions are characterized by extensive carbonate rock distribution and unique hydrogeological features, harboring an exceptionally high diversity of endemic species. Amphibians in these habitats often represent highly specialized taxa (Wang et al. 2019; Xu et al. 2024).

The genus *Odorrana* Fei, Ye & Huang, 1990, is widely distributed across high-gradient streams spanning Japan, southern China, the Indochinese Peninsula (extending westward to northeastern India, Myanmar, and Thailand), and southward through the Malay Peninsula to Sumatra and Borneo. Currently, 67 species within this genus have been documented globally (Frost 2025), among which some are strictly dependent on karst cave environments, exhibiting unique ecological adaptations (Mo et al. 2015; Luo et al. 2021; Lin et al. 2022; Song et al. 2025).

Recent advances in biological surveys of karst areas have led to the discovery of multiple new *Odorrana* species, all displaying distinct morphological traits and microhabitat specialization (Mo et al. 2015; Luo et al. 2021; Lin et al. 2022; Song et al. 2025). Studies suggest that geographic isolation and niche differentiation within karst caves are key drivers of rapid species radiation in this genus (Song et al. 2025). For instance, the *O. lipuensis* group,

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a basal clade of *Odorrana*, exclusively inhabits dark caves or humid limestone environments. Members of this group share synapomorphic traits such as the absence of vocal sacs and expanded digit tips, alongside pronounced genetic divergence (Lin et al. 2022; Song et al. 2025).

Despite being a core distribution area of karst landforms in China, Guizhou Province remains understudied in terms of cave amphibian diversity. The karst plateau in central Guizhou, characterized by intricate cave systems and a humid climate, provides ideal habitats for cave-dwelling organisms. In May 2025, during field surveys of karst caves in Xiuwen County and Jinsha County, we collected a series of morphologically distinct *Odorrana* specimens. Preliminary observations revealed consistent differences from known species in body coloration, digital morphology, and body size proportions. Integrating morphological comparisons, phylogenetic analyses, and geographic distribution data, we collectively confirm this population as a new species within the genus *Odorrana*.

Materials and methods

Sampling

Eight specimens, including four males and four females of the unnamed taxon, were collected from Xiuwen and Jinsha County, Guizhou Province, China (Fig. 1). The Animal Care and Use Committee of Guizhou University provided full approval for this research (number: EAE-GZU-2022-T115). All specimens were fixed in 10% buffered formalin for 10 h and then transferred to 75% ethanol. Tissue samples were preserved separately in 95% ethanol prior to fixation. Specimens are deposited in the Zoological Collection of Moutai Institute, a permanent institutional collection managed by the College of Food Engineering, Moutai Institute (MT), with accession numbers MT XW20250504001–005 and MT JS20250504001–003.

Molecular data and phylogenetic analyses

DNA was extracted from muscle tissue using a DNA extraction kit from Tiangen Biotech Co., Ltd. (Beijing). Two fragments of the mitochondrial 16S rRNA (16S) and cytochrome oxidase subunit I (COI) genes were amplified. For 16S, the primers P7 (5'-CGCCTGTTTACCAAAAACAT-3') and P8 (5'-CCGGTCTGAACTCAGATCACGT-3') were used (Simon et al. 1994), and for COI, Chmf4 (5'-TYTCWACWAAYCAYAAAGAYATCGG-3') and Chmr4 (5'-ACYTCRGGRTGRCCRAARAATCA-3') were used (Che et al. 2012). Gene fragments were amplified under the following conditions: an initial denaturing step at 95 °C for 4 min; 36 cycles of denaturing at 95 °C for 30 s, annealing at 52 °C (for 16S) or 47 °C (for COI) for 40 s, and extending at 72 °C for 70 s. Sequencing was conducted using an ABI3730 automated DNA sequencer by Shanghai DNA BioTechnologies Co., Ltd. (Shanghai, China). New sequences were deposited in GenBank (for GenBank accession numbers, see Table 1).

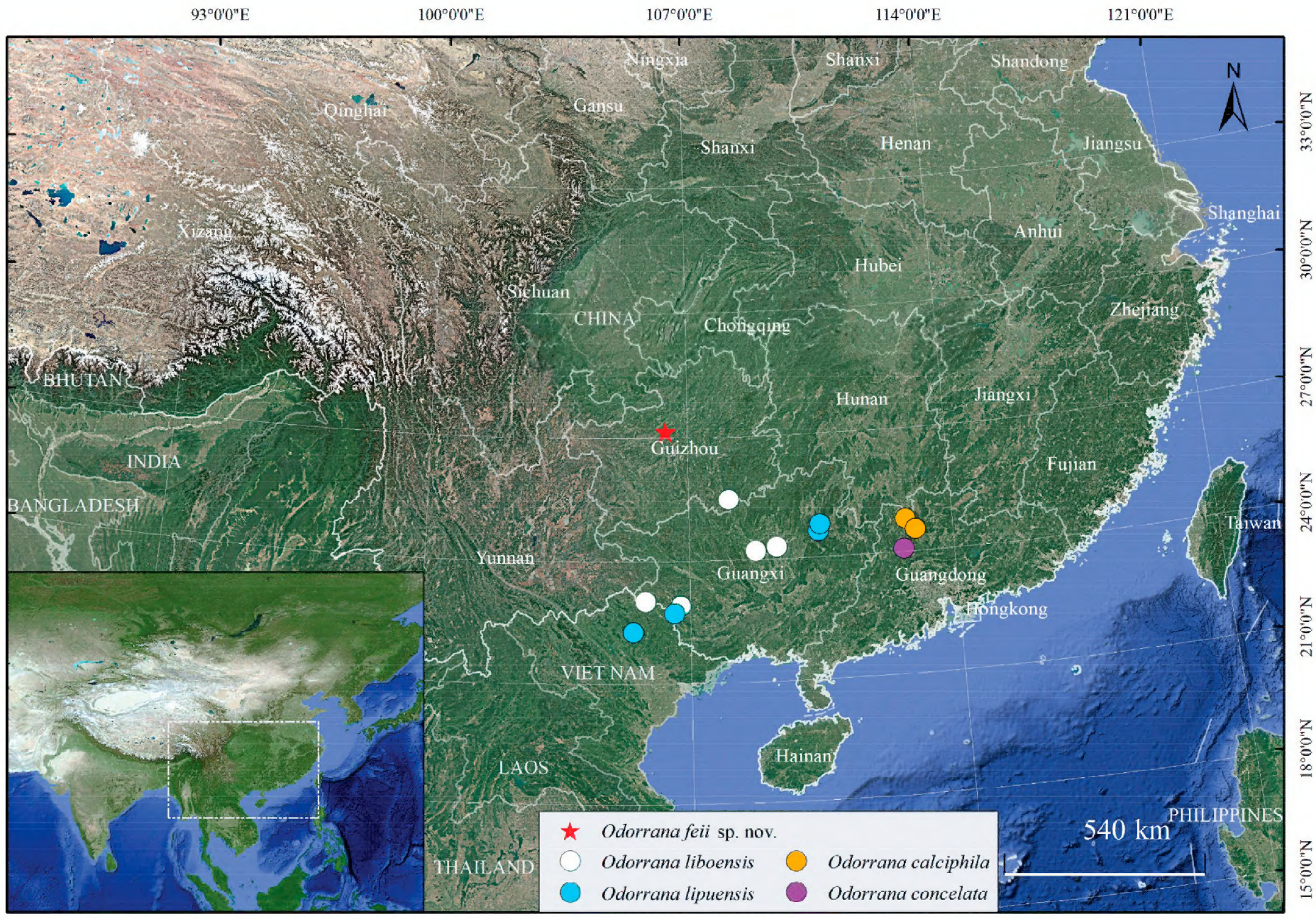

Figure 1. Map showing the distribution sites of *Odorrana feii* sp. nov. and its related species.

Table 1. Information for samples used in molecular phylogenetic analyses in this study.

ID	Species	Locality	Voucher ID	GenBank accession No.		Reference
				16S rRNA	CO1	
1	*Odorrana feii* **sp. nov.**	China: Guizhou: Xiuwen County	MT XW20250504001	PV951782	PV943472	This study
2	*Odorrana feii* **sp. nov.**	China: Guizhou: Xiuwen County	MT XW20250504002	PV951783	PV943473	This study
3	*Odorrana feii* **sp. nov.**	China: Guizhou: Xiuwen County	MT XW20250504003	PV951784	PV943474	This study
4	*Odorrana feii* **sp. nov.**	China: Guizhou: Jinsha County	MT JS20250504001	PV951785	PV943475	This study
5	*Odorrana feii* **sp. nov.**	China: Guizhou: Jinsha County	MT JS20250504002	PV951786	PV943476	This study
6	*Odorrana feii* **sp. nov.**	China: Guizhou: Jinsha County	MT JS20250504003	PV951787	PV943477	This study
7	*Odorrana lipuensis*	China: Guangxi: Lipu City: Maling Town	NHMG 1303018	MH665676	/	Luo et al. 2021
8	*Odorrana lipuensis*	China: Guangxi: Lipu City: Maling Town	NHMG 1303019	KM388701	/	Mo et al. 2015
9	*Odorrana lipuensis*	China: Guangxi: Yangshuo County: Yangshuo Town	SYS a004566	PV347087	PV341298	Song et al. 2025
10	*Odorrana lipuensis*	China: Guangxi: Yangshuo County: Yangshuo Town	SYS a004898	PV347088	PV341299	Song et al. 2025
11	*Odorrana lipuensis*	Vietnam: Cao Bang: Ha Lang District: Lung Tung Village	IEBR A.2015.63	LC155910	/	Pham et al. 2016a
12	*Odorrana lipuensis*	Vietnam: Cao Bang: Ha Lang District: Coong Village	IEBR A.2015.65	LC155911	/	Pham et al. 2016a
13	*Odorrana liboensis*	China: Guizhou: Libo County: Maolan Nature Reserve	GZNU 20180608007	MW481350	/	Luo et al. 2021
14	*Odorrana liboensis*	China: Guizhou: Libo County: Maolan Nature Reserve	SYS a008240	PV347080	PV341295	Song et al. 2025
15	*Odorrana liboensis*	China: Guangxi: Napo County: Nongyao Village	GXNU YU000307	ON514525	/	Mo et al. 2022
16	*Odorrana liboensis*	China: Guangxi: Daxin County: Xialei Town	SYS a003469	PV347079	PV341294	Song et al. 2025
17	*Odorrana liboensis*	China: Guangxi: Liuzhou City: Liunan District	SYS a008946	PV347084	PV341296	Song et al. 2025
18	*Odorrana liboensis*	China: Guangxi: Xincheng County: Masi Town	SYS a009224	PV347085	PV341297	Song et al. 2025
19	*Odorrana calciphila*	China: Guangdong: Yangshan County: Loushuiping Village	SYS a008923	PV347065	PV341279	Song et al. 2025
20	*Odorrana calciphila*	China: Guangdong: Yangshan County: Loushuiping Village	SYS a009287	PV347066	PV341280	Song et al. 2025
21	*Odorrana calciphila*	China: Guangdong: Yangshan County: Loushuiping Village	SYS a009288	PV347067	PV341281	Song et al. 2025
22	*Odorrana calciphila*	China: Guangdong: Yangshan County: Loushuiping Village	SYS a009289	PV347068	PV341282	Song et al. 2025
23	*Odorrana calciphila*	China: Guangdong: Yangshan County: Loushuiping Village	SYS a009290	PV347069	PV341283	Song et al. 2025
24	*Odorrana calciphila*	China: Guangdong: Ruyuan County: Datan River Nature Reserve	SYS a009295	PV347070	PV341284	Song et al. 2025
25	*Odorrana concelata*	China: Guangdong: Qingyuan City: Longlinchang Village	GEP a050	OP137167	/	Lin et al. 2022
26	*Odorrana concelata*	China: Guangdong: Qingyuan City: Longlinchang Village	GEP a052	OP137169	/	Lin et al. 2022
27	*Odorrana concelata*	China: Guangdong: Qingyuan City: Longlinchang Village	GEP a055	OP137172	/	Lin et al. 2022
28	*Odorrana confusa*	China: Guangdong: Shixing County: Chebaling Nature Reserve	SYS a008595	OR658982	OR659591	Song et al. 2023
29	*Odorrana exiliversabilis*	China: Fujian: Wuyishan City: Mt. Wuyi	SYS a005931	PV347072	PV341286	Song et al. 2025
30	*Odorrana nasuta*	China: Hainan: Wuzhishan City: Mt. Wuzhi	SYS a005296	PV347090	PV344500	Song et al. 2025
31	*Odorrana versabilis*	China: Guangxi: Longsheng County: Huaping Nature Reserve	SYS a005118	PV347094	PV344501	Song et al. 2025
32	*Odorrana nasica*	China: Yunnan: Xichou County: Fadou Town	SYS a008842	OR658988	OR659609	Song et al. 2023
33	*Odorrana yentuensis*	China: Guangxi: Shangsi County: Mt. Shiwandashan	SYS a003543	PV347095	PV341305	Song et al. 2025
34	*Odorrana damingshanensis*	China: Guangxi: Nanning City: Mt. Daming	NNU 00690	ON791420	ON791393	Chen et al. 2024
35	*Odorrana tormota*	China: Anhui: Huangshan City: Mt. Huangshan	SYS a002699	PV347093	PV341303	Song et al. 2025
36	*Odorrana amamiensis*	Japan: Kagoshima: Amami Island	KUHE 29529	AB200946	/	Matsui et al. 2005
37	*Odorrana narina*	Japan: Okinawa: Okinawa Island	/	AB511287	AB511288	Kurabayashi et al. 2010
38	*Odorrana supranarina*	Japan: Okinawa: Iriomote Island	KUHE 12898	AB200950	/	Matsui et al. 2005
39	*Odorrana swinhoana*	China: Taiwan: Nantou County	HNNU TW9	KF185046	/	Chen et al. 2013
40	*Odorrana utsunomiyaorum*	Japan: Okinawa: Ishigaki Island	KUHE 24144	AB200951	/	Matsui et al. 2005
41	*Odorrana aureola*	Thailand: Loei: Phu Luang County	ZMKU AM 01137	KT002162	/	Ampai et al. 2015
42	*Odorrana livida*	Thailand: Prachuap Khiri Khan: Thap Sakae District	THNHM 27263	MH079596	/	Rujirawan et al. 2018
43	*Odorrana chloronota*	China: Xizang: Medog County	SYS a008274	PV347071	PV341285	Song et al. 2025
44	*Odorrana graminea*	China: Hainan: Wuzhishan City: Mt. Wuzhi	SYS a005271	ON391778	ON381769	Lyu et al. 2024
45	*Odorrana leporipes*	China: Guangdong: Shaoguan City: Mt. Longtou	SYS a002769	PV347078	PV341293	Song et al. 2025
46	*Odorrana hosii*	Malaysia: Kuala Lumpur City	IABHU 21004	AB511284	AB511285	Kurabayashi et al. 2010
47	*Odorrana banaorum*	Vietnam: Gia Lai: An Khe County: Tram Lap	ROM 7472	AF206487	/	Chen et al. 2005
48	*Odorrana morafkai*	Vietnam: Gia Lai: An Khe County: Tram Lap	ROM 7446	AF206484	/	Chen et al. 2005
49	*Odorrana heatwolei*	Laos: Phongsaly: Phongsaly City	FMNH 258134	OR237216	/	Liu et al. 2023
50	*Odorrana tiannanensis*	China: Yunnan: Hekou County	KIZ 20193272	OL831009	/	Liu et al. 2023
51	*Odorrana macrotympana*	China: Yunnan: Yingjiang County	KIZ 2009051020	OL831010	/	Liu et al. 2023
52	*Odorrana fengkaiensis*	China: Guangdong: Fengkai County: Heishiding Nature Reserve	SYS a002160	KT315378	OR659600	Song et al. 2023

ID	Species	Locality	Voucher ID	GenBank accession No.		Reference
				16S rRNA	CO1	
53	*Odorrana hainanensis*	China: Hainan: Lingshui County: Mt. Diaoluo	SYS a007666	PV347073	PV341287	Song et al. 2025
54	*Odorrana bacboensis*	Vietnam: Nghe An: Con Cuong County: Khe Moi River	ROM 13044	AF206480	/	Wang et al. 2015
55	*Odorrana hejiangensis*	China: Sichuan: Hejiang County: Zihuai Town	SYS a004936	PV347074	PV341288	Song et al. 2023
56	*Odorrana ichangensis*	China: Hubei: Changyang County: Gaojiayan Town	SYS a005475	OR879765	PV341289	Li et al. 2024; Song et al. 2025
57	*Odorrana kweichowensis*	China: Guangxi: Nanning City: Mt. Daming	SYS a005210	PV347077	PV341292	Song et al. 2025
58	*Odorrana schmackeri*	China: Hubei: Changyang County: Gaojiayan Town	SYS a005478	PV347091	PV341301	Song et al. 2023
59	*Odorrana huanggangensis*	China: Fujian: Wuyishan City: Mt. Wuyi	SYS a004148	OR658951	OR659603	Song et al. 2023
60	*Odorrana tianmuii*	China: Zhejiang: Hangzhou City: Mt. Tianmu	SYS a006431	PV347092	PV341302	Song et al. 2025
61	*Odorrana leishanensis*	China: Guizhou: Leishan County: Mt. Leigong	MT LS20230806010	OR879754	/	Li et al. 2024
62	*Odorrana ishikawae*	Japan: Okinawa: Okinawa Island	KUHE 10069	AB200945	/	Matsui et al. 2005
63	*Odorrana splendida*	Japan: Kagoshima: Amami Island	IABHU 5275	AB511282	AB511282	Kurabayashi et al. 2010
64	*Odorrana chapaensis*	Vietnam: Lao Cai: Van Ban County: Nam Tha	AMNH 168686	EU861550	/	Bain et al. 2009
65	*Odorrana geminata*	Vietnam: Ha Giang: Vi Xuyen County: Cao Bo	AMNH 163782	EU861546	/	Bain et al. 2009
66	*Odorrana grahami*	China: Yunnan: Pingbian County: Mt. Dawei	SWFU 003918	MW551527	MW551527	Wen et al. 2021
67	*Odorrana jingdongensis*	China: Yunnan: Jingdong County: Xinmin Village	SYS a003922	PV347075	PV341290	Song et al. 2023
68	*Odorrana junlianensis*	China: Sichuan: Junlian County	HNNU 002JL	KF185058	/	Chen et al. 2013
69	*Odorrana yunnanensis*	China: Yunnan: Longchuan County	HNNU 001YN	KF185057	/	Chen et al. 2013
70	*Odorrana margaretae*	China: Sichuan: Emeishan City: Mt. Emei	SYS a005303	ON391779	ON381770	Lyu et al. 2024
71	*Odorrana kuangwuensis*	China: Sichuan: Nanjiang County: Mt. Guangwu	SYS a005409	PV347076	PV341291	Song et al. 2025
72	*Odorrana dulongensis*	China: Yunnan: Gongshan County: Dulongjiang Village	KIZ 035029	MW128104	/	Liu et al. 2021
73	*Odorrana mutschmanni*	Vietnam: Cao Bang: Ha Lang District: Coong Village	IEBR 3723	KU356765	/	Pham et al. 2016b
74	*Odorrana wuchuanensis*	China: Guangdong: Yangshan County: Jiangying Town	SYS a009109	PP388290	PV341304	Song et al. 2024; Song et al. 2025
75	*Odorrana lungshengensis*	China: Guangxi: Xing'an County: Mt. Maoer	SYS a002290	PV347089	PV341300	Song et al. 2025
76	*Odorrana yizhangensis*	China: Jiangxi: Jinggangshan City: Mt. Jinggang	SYS a004206	PV347096	PV341306	Song et al. 2025
77	*Odorrana anlungensis*	China: Guangxi: Tianlin County: Mt. Cenwanglaoshan	SYS a005974	PV347064	PV341278	Song et al. 2025
78	*Odorrana absita*	Laos: Xe Kong: Xe Sap	FMNH 258109	EU861542	/	Bain et al. 2009
79	*Babina holsti*	Japan: Okinawa: Okinawa Island	/	NC022870	NC022870	Kakehashi et al. 2013
80	*Babina subaspera*	Japan: Kagoshima: Amami Island	/	NC022871	NC022871	Kakehashi et al. 2013
81	*Nidirana adenopleura*	China: Taiwan: Taichung City	SYS a007365	ON391784	ON381775	Lyu et al. 2024
82	*Nidirana daunchina*	China: Sichuan: Emeishan City: Mt. Emei	SYS a004594	MF807822	MF807861	Lyu et al. 2017
83	*Rana hanluica*	China: Hunan: Shuangpai County: Mt. Yangming	SYS a001137	MT408956	MT418618	Wan et al. 2020
84	*Hylarana latouchii*	China: Fujian: Wuyishan City: Mt. Wuyi	SYS a001723	PV347062	/	Song et al. 2025
85	*Hylarana taipehensis*	China: Guangdong: Yangchun City: Ehuangzhang Nature Reserve	SYS a004695	PV347063	/	Song et al. 2025
86	*Glandirana tientaiensis*	China	/	KJ941041	KJ941041	Yan et al. 2016
87	*Pelophylax nigromaculatus*	Japan	/	AB043889	AB043889	Sumida et al. 2001
88	*Amolops ricketti*	China: Fujian: Wuyishan City: Mt. Wuyi	SYS a004141	MK263259	MG991927	Lyu et al. 2019
89	*Amolops chunganensis*	China: Jiangxi: Jinggangshan City: Mt. Jinggang	SYS a004213	MK263264	MG991915	Lyu et al. 2019

For phylogenetic and genetic divergence analyses, we downloaded available corresponding sequence data for all related species from GenBank according to previous studies (Song et al. 2025; Table 1). Sequences were assembled and aligned using the ClustalW module in BioEdit v.7.0.9.0 (Hall 1999) with default settings.

To assess phylogenetic signal and potential conflicts between the two mitochondrial genes, we used maximum likelihood (ML) and Bayesian inference (BI) methods on the individual 16S and COI datasets separately, as well as on the concatenated (16S + COI) dataset, implemented in PhyML 3.0 (Guindon et al. 2010) and MrBayes v.3.2.7 (Ronquist et al. 2012), respectively. To account for potential differences in evolutionary rates and patterns among genes and codon positions, phylogenetic analyses were performed using partitioned models: 16S rRNA as one partition and COI divided into three partitions by codon positions (1st, 2nd, and 3rd). The best-fit substitution models for each partition (GTR + G + I for 16S, GTR + G for COI 1st, HKY + I for COI 2nd, and GTR + G for COI 3rd) were selected by PartitionFinder 2 (Lanfear et al. 2012).

For ML analyses conducted in PhyML 3.0, the bootstrap consensus tree inferred from 1000 replicates was used to estimate nodal supports of inferred relationships on phylogenetic trees. For Bayesian analyses conducted in MrBayes 3.2.7, four Markov chains were run for 50 million generations with sampling every 1000 generations. Convergence was assessed by monitoring the average standard deviation of split frequencies (< 0.01), following recommendations in the MrBayes manual (Ronquist et al. 2012). The first 25% of trees were removed as the burn-in stage, followed by calculation of Bayesian posterior probabilities and the 50% majority-rule consensus of the post–burn-in trees sampled at stationarity. Finally, uncorrected p-distances (1000 replicates) between species based on 16S and COI were calculated in MEGA 6.06 (Tamura et al. 2013). Genetic distances within the newly described species were calculated separately for specimens from each cave.

Morphological comparisons

Morphological measurements were made with dial calipers to the nearest 0.1 mm by Shize Li, following Fei et al. (2009) and Song et al. (2025). Eighteen morphometric characters of eight adult specimens were measured (Suppl. material 1), abbreviated as follows: ED (eye diameter, distance from the anterior corner to the posterior corner of the eye), FL (foot length, distance from tarsus to the tip of fourth toe), F3W (finger III disc width, horizontal maximum between both sides), HDL (head length, distance from the tip of the snout to the articulation of jaw), HDW (maximum head width, greatest width between the left and right articulations of jaw), IND (internasal distance, minimum distance between the inner margins of the external nares), IOD (interorbital distance, minimum distance between the inner edges of the upper eyelids), LAL (length of lower arm and hand, distance from the elbow to the distal end of finger IV), LW (lower arm width, maximum width of the lower arm), ML (manus length, distance from tip of third digit to proximal edge of inner palmar tubercle), TFL (length of foot and tarsus, distance from the tibiotarsal articulation to the distal end of toe IV), THL (thigh length, distance from vent to knee), TL (tibia length, distance from knee to tarsus), TW (maximum tibia width), TYD (maximum tympanum diameter), SL (snout length, distance from the tip of the snout to the anterior corner of the eye), SVL (snout–vent length, distance from the tip of the snout to the posterior edge of the vent), UEW (upper eyelid width, greatest width of the upper eyelid margins measured perpendicular to the anterior–posterior axis).

Sex was determined by examination of primary sexual characteristics after dissection. Additional morphological data used for comparisons were obtained from the literature (Table 2).

Results

Phylogenetic analyses

A total of 540 base pairs (bp) of the 16S gene and 590 bp of the COI gene were sequenced. To assess phylogenetic signal and potential conflicts between these genes, we conducted separate ML and BI analyses on the individual 16S and COI datasets, as well as on the concatenated (16S + COI) dataset. While the individual gene trees (Suppl. materials 4, 5) showed largely congruent topologies regarding major clades and the placement of the undescribed taxon, the concatenated analysis yielded stronger nodal support for key relationships and resolved minor topological ambiguities present in the single-gene trees. Therefore, based on this assessment and considering the established utility of mitochondrial markers for species delimitation in this group—especially given clear morphological evidence and resource limitations—we proceeded with the concatenated dataset for our final phylogenetic inferences to maximize resolution and support. Both BI and ML analyses yielded highly congruent topologies, with most nodes strongly supported (BPP ≥ 0.95; BS ≥ 70). Discordant branching patterns were restricted to a few weakly supported nodes (BPP < 0.95 and BS < 70) within the genus *Odorrana*. The undescribed taxon was supported as the sister lineage to *O. lipuensis* in all analyses (BPP = 0.99, BS = 80) (Fig. 2). This species is highly divergent from the latter in terms of genetic distance, with a minimum pairwise divergence of 2.6% and 4.4%, calculated based on the 16S and COI genes, respectively. These values are much higher than those between many other pairs of species in the genus (Suppl. materials 2, 3). Furthermore, these specimens are distinguishable from other congeners within the genus by a unique combination of morphological characters (see taxonomic account below).

Morphological comparisons

Morphological data used for comparisons were obtained from the literature (Table 2). Based on phylogenetic analysis places the undescribed taxon within the *Odorrana lipuensis* group as a sister lineage to *O. lipuensis*. However, the undescribed taxon can be morphologically distinguished from its congeners by the following characteristics (Table 3): From *O. lipuensis*, smaller male body size (37.0–39.0 mm vs. 40.7–49.8 mm); presence of a dorsolateral fold in adult females (vs. absent in both sexes); sparse or absent dorsolateral conical spines (vs. dense); relative finger length I < II (vs. II ≤ I). From *Odorrana liboensis*, smaller male body size (37.0–39.0 mm vs. 43.7–53.8 mm); tibiotarsal articulation reaching the nostril when the leg is stretched forward (vs. between eye and nostril); distinct dorsal band (vs. indistinct). From *O. calciphila*, larger female body size (49.4–52.2 mm vs. 39.9–45.7 mm); tibiotarsal articulation reaching the nostril

Table 2. References for morphological characters for congeners of the genus *Odorrana*.

ID	Species	Reference
1	*Odorrana absita* (Stuart & Chan-ard, 2005)	Stuart and Chan-Ard 2005
2	*Odorrana amamiensis* (Matsui, 1994)	Matsui 1994
3	*Odorrana anlungensis* (Liu & Hu, 1973)	Hu et al. 1973
4	Odorrana arunachalensis Saikia, Sinha & Kharkongor, 2017	Saikia et al. 2017
5	*Odorrana aureola* Stuart, Chuaynkern, Chan-ard & Inger, 2006	Stuart et al. 2006
6	*Odorrana bacboensis* (Bain, Lathrop, Murphy, Orlov & Ho, 2003)	Bain et al. 2003
7	*Odorrana banaorum* (Bain, Lathrop, Murphy, Orlov & Ho, 2003)	Bain et al. 2003
8	*Odorrana bolavensis* (Stuart & Bain, 2005)	Stuart and Bain 2005
9	*Odorrana calciphila* Song, Qi, Wang, Liu & Wang, 2025	Song et al. 2025
10	*Odorrana cangyuanensis* (Yang, 2008)	Yang and Rao 2008
11	*Odorrana chapaensis* (Bourret, 1937)	Bain et al. 2009
12	*Odorrana chloronota* (Günther, 1876)	Bain et al. 2003
13	*Odorrana concelata* Wang, Zeng & Lin, 2022	Lin et al. 2022; Song et al. 2025
14	*Odorrana confusa* Song, Zhang, Qi, Lyu, Zeng & Wang, 2023	Song et al. 2023
15	*Odorrana damingshanensis* Chen, Mo, Lin & Qin, 2024	Chen et al. 2024
16	*Odorrana dulongensis* Liu, Che & Yuan, 2021	Liu et al. 2021
17	*Odorrana exiliversabilis* Li, Ye & Fei, 2001	Fei et al. 2001b
18	*Odorrana fengkaiensis* Wang, Lau, Yang, Chen, Liu, Pang & Liu, 2015	Wang et al. 2015
19	*Odorrana geminata* Bain, Stuart, Nguyen, Che & Rao, 2009	Bain et al. 2009
20	*Odorrana gigatympana* (Orlov, Ananjeva & Ho, 2006)	Orlov et al. 2006
21	*Odorrana grahami* (Boulenger, 1917)	Boulenger 1917
22	*Odorrana graminea* (Boulenger, 1900)	Boulenger 1900
23	*Odorrana hainanensis* Fei, Ye & Li, 2001	Fei et al. 2001a
24	*Odorrana heatwolei* (Stuart & Bain, 2005)	Stuart and Bain 2005
25	*Odorrana hejiangensis* (Deng & Yu, 1992)	Deng and Yu 1992
26	*Odorrana hosii* (Boulenger, 1891)	Boulenger 1920
27	*Odorrana huanggangensis* Chen, Zhou & Zheng, 2010	Chen et al. 2010b
28	*Odorrana ichangensis* Chen, 2020	Shen et al. 2020
29	*Odorrana indeprensa* (Bain & Stuart, 2006)	Bain and Stuart 2006
30	*Odorrana ishikawae* (Stejneger, 1901)	Stejneger 1901; Kuramoto et al. 2011
31	*Odorrana jingdongensis* Fei, Ye & Li, 2001	Fei et al. 2001a
32	*Odorrana junlianensis* Huang, Fei & Ye, 2001	Fei et al. 2009
33	*Odorrana khalam* (Stuart, Orlov & Chan-ard, 2005)	Stuart et al. 2005
34	*Odorrana kuangwuensis* (Liu & Hu, 1966)	Hu et al. 1966
35	*Odorrana kweichowensis* Li, Xu, Lv, Jiang, Wei & Wang, 2018	Li et al. 2018
36	*Odorrana leishanensis* Li, Chen, Su, Liu, Tang & Wang, 2024	Li et al. 2024
37	*Odorrana leporipes* (Werner, 1930)	Bain et al. 2003
38	*Odorrana liboensis* Luo, Wang, Xiao, Wang & Zhou, 2021	Luo et al. 2021; Mo et al. 2022; Song et al. 2025
39	*Odorrana lipuensis* Mo, Chen, Wu, Zhang & Zhou, 2015	Mo et al. 2015; Pham et al. 2016a; Song et al. 2025
40	*Odorrana livida* (Blyth, 1856)	Bain et al. 2003
41	*Odorrana lungshengensis* (Liu & Hu, 1962)	Liu and Hu 1962
42	*Odorrana macrotympana* (Yang, 2008)	Yang and Rao 2008
43	*Odorrana margaretae* (Liu, 1950)	Liu 1950; Fei et al. 2009
44	*Odorrana mawphlangensis* (Pillai & Chanda, 1977)	Pillai and Chanda 1977; Mahony 2008
45	*Odorrana monjerai* (Matsui & Jaafar, 2006)	Matsui and Jaafar 2006
46	*Odorrana morafkai* (Bain, Lathrop, Murphy, Orlov & Ho, 2003)	Bain et al. 2003
47	*Odorrana mutschmanni* Pham, Nguyen, Le, Bonkowski & Ziegler, 2016	Pham et al. 2016b
48	*Odorrana nanjiangensis* Fei, Ye, Xie & Jiang, 2007	Fei et al. 2007b
49	*Odorrana narina* (Stejneger, 1901)	Matsui 1994
50	*Odorrana nasica* (Boulenger, 1903)	Boulenger 1903
51	*Odorrana nasuta* Li, Ye & Fei, 2001	Fei et al. 2001b
52	*Odorrana orba* (Stuart & Bain, 2005)	Stuart and Bain 2005
53	*Odorrana sangzhiensis* Zhang, Li, Hu & Yang, 2021	Zhang et al. 2021
54	*Odorrana schmackeri* (Boettger, 1892)	Shen et al. 2020
55	*Odorrana sinica* (Ahl, 1927)	Bain et al. 2003
56	*Odorrana splendida* Kuramoto, Satou, Oumi, Kurabayashi & Sumida, 2011	Kuramoto et al. 2011
57	*Odorrana supranarina* (Matsui, 1994)	Matsui 1994
58	*Odorrana swinhoana* (Boulenger, 1903)	Boulenger 1903
59	*Odorrana tianmuii* Chen, Zhou & Zheng, 2010	Chen et al. 2010a
60	*Odorrana tiannanensis* (Yang & Li, 1980)	Yang and Li 1980
61	*Odorrana tormota* (Wu, 1977)	Herpetological Department, Sichuan Biological Research Institute 1977
62	*Odorrana utsunomiyaorum* (Matsui, 1994)	Matsui 1994

ID	Species	Reference
63	*Odorrana versabilis* (Liu & Hu, 1962)	Liu and Hu 1962
64	*Odorrana wuchuanensis* (Xu, 1983)	Wu et al. 1983
65	*Odorrana yentuensis* Tran, Orlov & Nguyen, 2008	Tran et al. 2008
66	*Odorrana yizhangensis* Fei, Ye & Jiang, 2007	Fei et al. 2007a
67	*Odorrana yunnanensis* Anderson, 1879	Fei et al. 2009

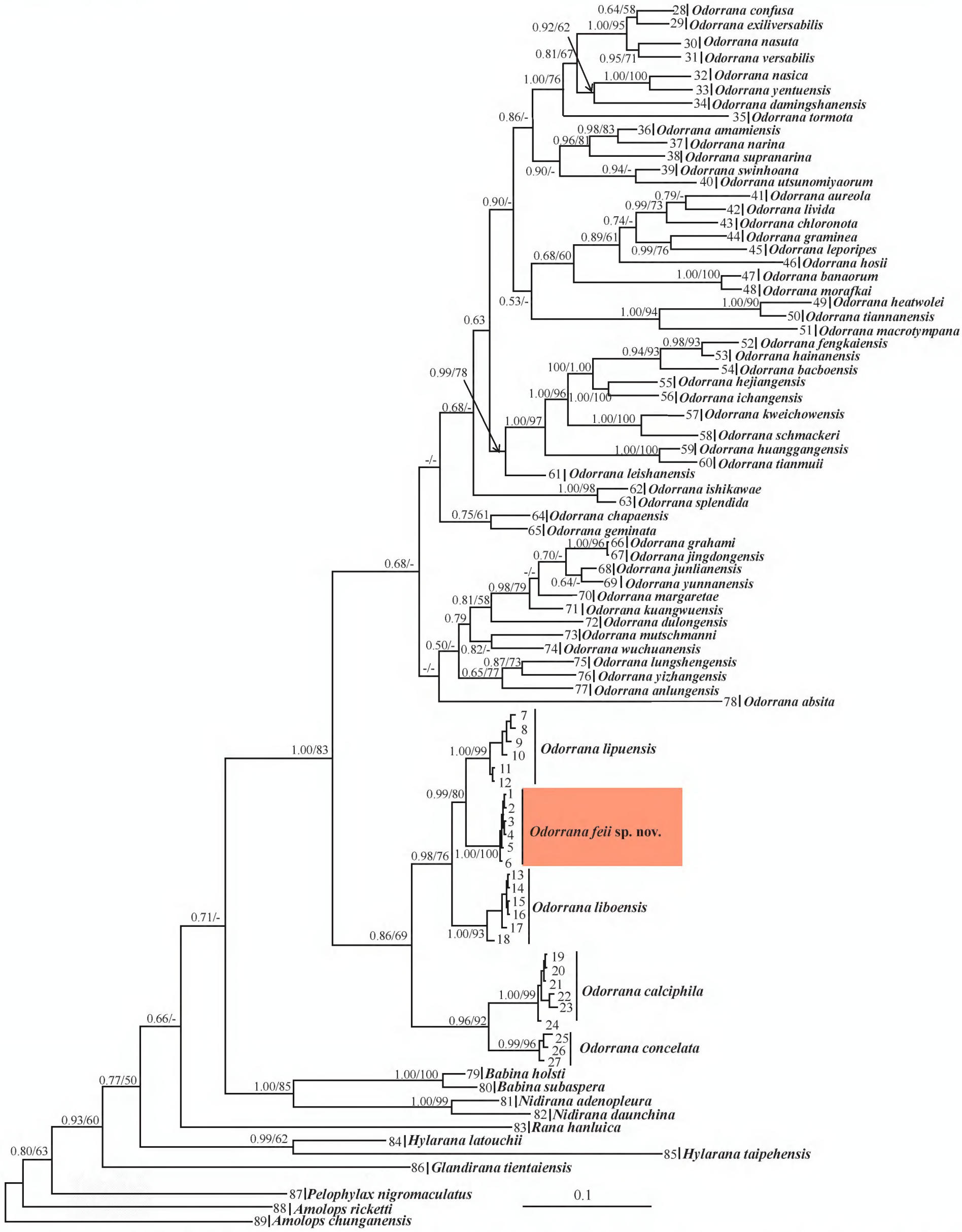

Figure 2. BI tree of the genus *Odorrana* was reconstructed based on the 16S and COI gene sequences. Bayesian posterior probability/ML bootstrap supports were denoted beside each node, and "-" denotes BS < 50% or BPP < 0.60. Samples 1–89 refer to Table 1.

Table 3. Diagnostic characters separating *Odorrana feii* sp. nov. from its related species.

Morphological character	*Odorrana feii* sp. nov.	*O. calciphila*	*O. concelata*	*O. liboensis*	*O. lipuensis*
SVL in adult male (in mm)	37.0–39.0	37.9	33.9–36.8	43.7–53.8	40.7–49.8
SVL in adult female (in mm)	49.4–52.2	39.9–45.7	41.3–46.0	48.8–58.2	49.9–60.1
Relative finger length	I < II	I < II	II ≤ I	I < II	II ≤ I
Dorsolateral conical spine	Sparse or absent	Dense, sparse or absent	Dense or sparse	Sparse or absent	Dense
Tibiotarsal articulation (when stretched)	Reaching nostril	Exceeding nostril	Reaching nostril	Between eye and nostril	Reaching nostril
Dorsolateral fold	Present in adult females and absent in adult males	Prominent and swollen in adult females and absent in adult male	Absent in both sexes	Present in adult females and present or absent in adult males	Absent in both sexes
Band on the dorsal surface of hind-limb	Clear	Clear	Clear	Unclear	Clear

(vs. exceeding nostril). From *O. concelata*, larger female body size (49.4–52.2 mm vs. 41.3–46.0 mm); presence of dorsolateral fold in adult females (vs. absent in both sexes); relative finger length I < II (vs. II ≤ I).

The undescribed taxon differs from other congeners by the absence of the vocal sac in males (vs. present in *Odorrana absita*, *O. amamiensis*, *O. anlungensis*, *O. aureola*, *O. bacboensis*, *O. banaorum*, *O. bolavensis*, *O. cangyuanensis*, *O. chapaensis*, *O. chloronota*, *O. confusa*, *O. damingshanensis*, *O. dulongensis*, *O. exiliversabilis*, *O. fengkaiensis*, *O. geminata*, *O. gigatympana*, *O. grahami*, *O. graminea*, *O. hainanensis*, *O. heatwolei*, *O. hejiangensis*, *O. hosii*, *O. huanggangensis*, *O. ichangensis*, *O. indeprensa*, *O. ishikawae*, *O. jingdongensis*, *O. junlianensis*, *O. khalam*, *O. kweichowensis*, *O. leporipes*, *O. livida*, *O. lungshengensis*, *O. macrotympana*, *O. monjerai*, *O. morafkai*, *O. nanjiangensis*, *O. nasica*, *O. nasuta*, *O. orba*, *O. sangzhiensis*, *O. schmackeri*, *O. supranarina*, *O. swinhoana*, *O. tianmuii*, *O. tiannanensis*, *O. tormota*, *O. utsunomiyaorum*, *O. versabilis*, *O. yentuensis*, *O. yizhangensis*, and *O. yunnanensis*).

By having medium body size (maximum SVL < 40.0 mm in males), the undescribed taxon differs from *Odorrana amamiensis*, *O. aureola*, *O. bacboensis*, *O. banaorum*, *O. bolavensis*, *O. cangyuanensis*, *O. chapaensis*, *O. chloronota*, *O. confusa*, *O. damingshanensis*, *O. dulongensis*, *O. exiliversabilis*, *O. geminata*, *O. grahami*, *O. graminea*, *O. hainanensis*, *O. hejiangensis*, *O. hosii*, *O. huanggangensis*, *O. ishikawae*, *O. indeprensa*, *O. jingdongensis*, *O. junlianensis*, *O. kuangwuensis*, *O. leporipes*, *O. liboensis*, *O. lipuensis*, *O. lungshengensis*, *O. macrotympana*, *O. margaretae*, *O. mawphlangensis*, *O. mutschmanni*, *O. nanjiangensis*, *O. narina*, *O. nasica*, *O. nasuta*, *O. sangzhiensis*, *O. schmackeri*, *O. splendida*, *O. supranarina*, *O. swinhoana*, *O. tianmuii*, *O. tiannanensis*, *O. versabilis*, *O. wuchuanensis*, *O. yentuensis*, *O. yizhangensis*, and *O. yunnanensis* (vs. minimum SVL > 40.0 mm).

By having medium body size (maximum SVL < 55.0 mm in females), the undescribed taxon differs from *Odorrana amamiensis*, *O. anlungensis*, *O. arunachalensis*, *O. aureola*, *O. bacboensis*, *O. banaorum*, *O. bolavensis*, *O. chapaensis*, *O. chloronota*, *O. confusa*, *O. damingshanensis*, *O. dulongensis*, *O. fengkaiensis*, *O. geminata*, *O. grahami*, *O. hainanensis*, *O. heatwolei*, *O. hejiangensis*, *O. hosii*, *O. huanggangensis*, *O. ichangensis*, *O. indeprensa*, *O. ishikawae*, *O. jingdongensis*, *O. junlianensis*, *O. kuangwuensis*, *O. kweichowensis*, *O. livida*, *O. lungshengensis*, *O. macrotympana*, *O. margaretae*, *O. monjerai*, *O. morafkai*, *O. mutschmanni*, *O. nanjiangensis*, *O. nasica*, *O. narina*, *O. nasuta*, *O. orba*, *O. sangzhiensis*, *O. schmackeri*, *O. splendida*, *O. supranarina*, *O. swinhoana*, *O. tiannanensis*, *O. versabilis*, *O. wuchuanensis*, *O. yentuensis*, *O. yizhangensis*, and *O. yunnanensis* (vs. maximum SVL > 55.0 mm).

Taxonomic accounts

Adopting an integrative taxonomic approach that combines evidence from molecular phylogenetics and detailed morphological comparisons, we conclude that the specimen represents a lineage distinct from all other congeners of *Odorrana*. The description of this new species is provided below.

Odorrana feii sp. nov.

https://zoobank.org/AC7B6A72-AB77-4CC8-A52F-DBFCBBB9122A

Holotype. • MT XW20250504001 (Figs 3, 4), adult male, from Xiuwen County, Guizhou Province, China (27.136°N, 106.421°E, ca. 1100 m a.s.l.), collected by Shize Li on 4 May 2025.

Paratype. • Two male specimens, MT XW20250504004 and MT XW20250504005, and two female specimens, MT XW20250504002 and MT XW20250504003, collected on 4 May 2025 by Shize Li from the same place as the holotype, and three specimens, including one male (MT JS20250504001) and two female (MT JS20250504002 and MT JS20250504003), collected on 4 May 2025 by Lang Mu from Jinsha County, Guizhou Province, China (27.160°N, 106.414°E, ca. 980 m a.s.l.).

Etymology. The specific epithet 'Feii' is in commemoration of Fei Liang, a renowned Chinese herpetological taxonomist who made significant contributions to the study of the genus *Odorrana*. For the common English name "Fei's Odorous Frog" and Chinese name "Fei Shi Chou Wa (费氏臭蛙)".

Diagnosis. *Odorrana feii* sp. nov. is assigned to the genus *Odorrana* based upon molecular phylogenetic

analyses and the following morphological characters: (1) dorsum is mostly green; (2) tips of digits dilated, tapering, disks with circum-marginal grooves or lateroventral grooves, and vertical diameter longer than horizontal diameter in the disks; (3) supernumerary tubercle below the base of fingers III and IV; (4) feet fully webbed to disks, without tarsal fold; (5) dorsal skin smooth, dorsolateral folds absent or fine (Fei et al. 2009; Li et al. 2018).

Odorrana feii sp. nov. is distinguished from congeners by a combination of the following characters: (1) having medium body size (SVL 37.0–39.0 mm in males and 49.4–52.2 mm in females); (2) tympanum distinctly visible, greater than one-half the diameter of the eye; (3) dorsolateral folds absent in males; (4) relative finger lengths: I < II < IV < III; (5) tibiotarsal articulation reaching the nostril when the leg is stretched forward; (6) bands on the dorsal surface of hind-limb clear; and (7) vocal sacs absent in males.

Description of holotype. Adult male, body size moderate (SVL 38.5 mm); head length larger than head width slightly (HDW/HDL = 1.05); snout short, rounded in dorsal view, projecting beyond lower jaw; eye large and convex, ED 0.89 times of SL; nostril rounded, closer to tip of snout than to eye; internasal distance larger than interorbital distance, slightly; tympanum rounded and large, approximately 0.73 times of ED; vomerine teeth on well-developed ridges; tongue deeply notched posteriorly; vocal sac absent.

Forelimb slender; finger slender, relative finger length I < II < IV < III; tips of fingers II, III, and IV expanded into discs with lateroventral grooves, tip of finger I without grooves; fingers without webbing or lateral fringe; subarticular tubercle prominent, 1, 1, 2, and 2 on fingers I to IV, respectively; supernumerary tubercle below the base of finger small and indistinct; metacarpal tubercles three, the inner one oblong and outer two rounded.

Hindlimb long, tibiotarsal articulation reaching nostril when hind-limb stretched along the side of body, heels overlapping when hind-limbs flexed at right angles to the axis of body; toe slender, relative toe length I < II < III < V < IV; toes entirely webbed; tip of each toe expanded into oval disc, with lateroventral groove; subarticular tubercle prominent, 1, 1, 2, 3, and 2 on toes I to V, respectively; inner metatarsal tubercle prominent, oval, and elongated; outer metatarsal tubercle and tarsal fold absent.

Dorsal and ventral skin smooth, tiny spinules on lateral body; supratympanic fold short, distinct; dorsolateral fold absent; some flattened tubercles scattered on the rear of thigh and surrounding cloacae.

Color of holotype in life. Dorsal parts of head and dorsum, forelimb, thigh, tibia, and foot grass-green with irregular brown mottling; iris black, with golden speckles; tympanum brown; flank brown to light green, with white mottles; throat, chest, and abdomen white with pink; ventral surfaces of limbs pink; dorsal surfaces of limbs with brown bands.

Coloration of holotype in preservation. After three months in 75% ethanol, the dorsal surface of the head, body, and limbs faded to dark brown; the transverse bands on limbs and digits brown; ventral surface of throat brown, and chest with brown mottles; belly and palm faded to light yellow.

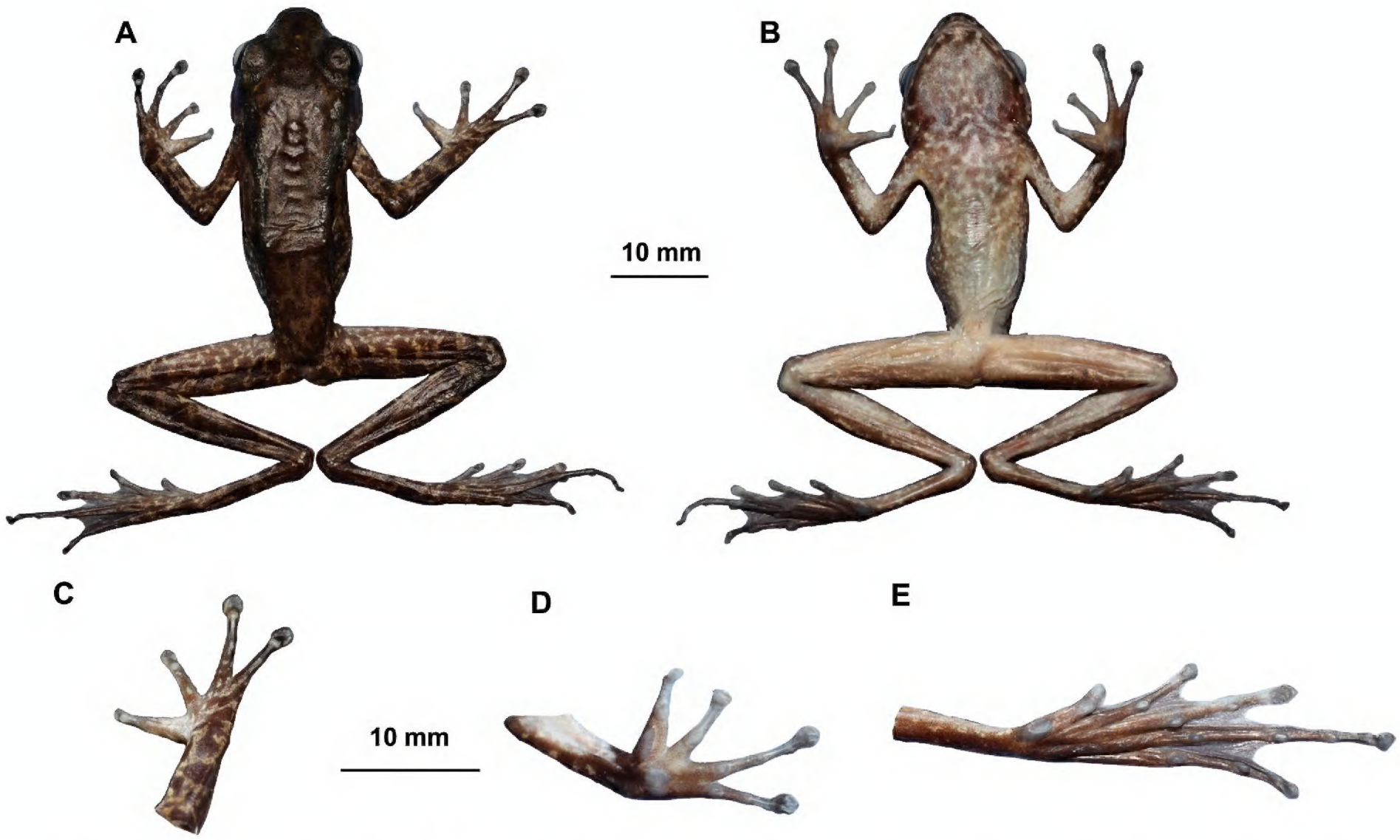

Figure 3. The holotype specimen MT XW20250504001 of *Odorrana feii* sp. nov. (preserved) in **A.** Dorsal view; **B.** Ventral view; **C.** Dorsal view of hand; **D.** Ventral view of hand; **E.** Ventral view of foot. (photos **A–E** by Shize Li).

Figure 4. Photographs of the holotype MT XW20250504001 of *Odorrana feii* sp. nov. in life. **A.** Dorsal view; **B.** Ventral view; **C.** Dorsal view of hand; **D.** Ventral view of hand; **E.** Ventral view of foot. (photos **A–E** by Shize Li).

Variation. Measurements of the type series are summarized in Table 4 and Suppl. material 1. All paratypes resemble the holotype in overall morphology, except for the following variations: in MT XW20250504002, brown patches on the dorsum and bands on dorsal limb surfaces are more reddish (Fig. 5A); in MT JS20250504002, brown patches on the dorsum are denser (Fig. 5B); in MT JS20250504003, the dorsolateral fold is distinct, tiny spinules on the lateral body are dense, and ventral limb surfaces possess grass-green patches (Fig. 5C, D).

Secondary sexual character. Adult females are larger than the adult males and have prominent and swollen dorsolateral folds; nuptial pads and nuptial spines were not found in adult males.

Distribution and habitats. At present, *Odorrana feii* sp. nov. is known only from caves in Xiuwen County and Jinsha County, Guizhou Province, China (Fig. 1). The distance between the two populations is approximately 5 km, and they are separated by a large river (Yachi River). It is therefore hypothesized that the species may be distributed throughout this region characterized by well-developed karst caves (Fig. 6). Both caves inhabited by the populations have water flowing out to the exterior (Fig. 6B). Individuals of this species are observed at the cave entrances at dusk; however, no other amphibian species have been found in the vicinity of these caves.

Table 4. Measurements of the eight adult male specimens of *Odorrana feii* sp. nov. Units are given in mm. See abbreviations for the morphological characters in the Materials and methods section.

Character	Male(n = 4)		Female(n = 4)	
	Range	mean ± SD	Range	mean ± SD
ED	5.1–5.7	5.5 ± 0.3	5.2–6.2	5.8 ± 0.4
FL	19.6–21.7	20.8 ± 1.0	25.9–26.6	26.2 ± 0.3
F3W	1.2–2.0	1.5 ± 0.4	1.8–2.4	2.1 ± 0.3
HDL	13.4–14.0	13.7 ± 0.3	15.6–16.9	16.4 ± 0.6
HDW	12.1–13.0	12.6 ± 0.4	16.2–17.1	16.7 ± 0.4
IND	4.2–4.7	4.4 ± 0.2	5.2–5.6	5.4 ± 0.2
IOD	4.0–4.5	4.2 ± 0.2	5.1–5.4	5.2 ± 0.1
LAL	19.6–20.3	19.9 ± 0.3	25.0–26.5	25.9 ± 0.7
LW	2.2–3.2	2.5 ± 0.5	3.0–3.4	3.2 ± 0.2
ML	10.6–11.9	11.4 ± 0.6	14.7–15.4	15.1 ± 0.3
SL	5.8–6.4	6.2 ± 0.3	6.9–7.8	7.5 ± 0.4
SVL	37.0–39.0	37.9 ± 1.0	49.4–52.2	50.7 ± 1.2
TFL	27.9–30.6	29.3 ± 1.5	35.4–37.9	36.7 ± 1.0
THL	17.5–20.3	19 ± 1.2	22.8–25.4	24.2 ± 1.1
TL	19.8–22.1	21.2 ± 1.1	25.9–27.5	26.5 ± 0.7
TW	3.2–3.4	3.4 ± 0.1	3.8–5.2	4.4 ± 0.7
TYD	3.4–4.4	3.9 ± 0.5	4.3–5.0	4.6 ± 0.3
UEW	3.0–3.7	3.2 ± 0.3	3.1–4.1	3.6 ± 0.5

Discussion

The discovery of *Odorrana feii* sp. nov. highlights the role of karst landscapes as evolutionary incubators for amphibian diversification in southern China (Xu et al. 2024). As a cave-obligate lineage nested within the *O. lipuensis* group, this species exemplifies the trend of microhabitat specialization driven by geographic isolation in karst systems (Wen et al. 2022). Its sister relationship to *O. lipuensis* (BPP = 0.99, BS = 80), coupled with significant genetic divergence (2.6% in 16S and 4.4% in COI), supports its status as an independent evolutionary unit. Notably, these distances exceed thresholds observed between many recognized *Odorrana* congeners (Suppl. materials 2, 3), reinforcing the efficacy of molecular markers in delimiting cryptic karst-adapted taxa (Cheng et al. 2025).

Figure 5. Color variation in *Odorrana feii* sp. nov. **A.** Dorsolateral view of the female specimen MT XW20250504002; **B.** Dorsolateral view of the female specimen MT JS20250504003; **C.** Dorsolateral view and **D.** Ventral view of female specimen MT JS20250504003. (photos **A–D** by Shize Li).

Figure 6. Habitats of *Odorrana feii* sp. nov. **A.** Landscape of the type locality, Xiuwen County, Guizhou Province, China; **B.** Waterfall outside the cave of the type locality; **C.** Views within the cave of the type locality; **D.** Views within the cave of Jinsha County, Guizhou Province, China. (photos **A–D** by Shize Li).

Odorrana feii sp. nov. exhibits several traits consistent with troglophilic ecology. The loss of vocal sacs, a synapomorphy of the *O. lipuensis* group, likely reflects reduced reliance on acoustic communication in echoic cave environments. Dorsal green coloration with irregular brown mottling provides camouflage in moss-covered, dimly lit cave entrances; expanded digital discs enhance grip on wet limestone substrates; and fully webbed feet facilitate locomotion in aquatic cave channels. The absence of dorsolateral folds in males (with presence in some females) suggests sexual dimorphism linked to microhabitat partitioning, though further behavioral studies are needed.

The species' disjunct distribution, separated by the Yachi River and confined to two caves 5 km apart, and low intraspecific uncorrected p-distances within *Odorrana feii* sp. nov. (0% for 16S and 0.1% for COI; Suppl. materials 2, 3), support the conspecificity of the two populations (Xiuwen and Jinsha counties) and indicate strong geographic isolation as a driver of speciation (Zhao et al. 2022; Li et al. 2025). Given the extensive karst networks in central Guizhou, we hypothesize that *Odorrana feii* sp. nov. may occur in other cave systems across the region. However, its apparent absence from surrounding surface habitats implies strict ecological dependence on cave microclimates (e.g., stable humidity, low light). The lack of sympatric amphibians further suggests niche exclusivity or competitive exclusion in these specialized environments.

As a microendemic with only two known populations, *Odorrana feii* sp. nov. faces critical threats from karst habitat degradation (Fig. 6C), climate change–induced hydrologic shifts altering cave moisture regimes, and extremely limited dispersal capacity due to river barriers and terrestrial unsuitability. Therefore, urgent surveys of adjacent karst towers are needed to assess its full distribution. We recommend provisional IUCN Red List status as Endangered (EN B1ab(iii)+2ab(iii)) based on extent of occurrence <100 km^2, severely fragmented habitat, and declining environmental quality (IUCN 2011).

While our integrated evidence robustly supports *Odorrana feii* sp. nov. as a new species, genomic data (e.g., RAD-seq) would clarify intraspecific structure between the Xiuwen and Jinsha populations. Additionally, bioacoustic analysis of its communication in acoustically limited cave environments and investigations into larval ecology (e.g., adaptations to oligotrophic cave streams) are future priorities.

Acknowledgements

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Supplementary material 1

Supplementary table S1

Authors: Shize Li, Lang Mu, Jiahao Jing, Jing Liu, Yanlin Cheng, Bin Wang
Data type: xlsx
Explanation note: Measurements of the adult specimens of *Odorrana feii* sp. nov.
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Link: https://doi.org/10.3897/zse.101.161151.suppl1

Supplementary material 2

Supplementary table S2

Authors: Shize Li, Lang Mu, Jiahao Jing, Jing Liu, Yanlin Cheng, Bin Wang
Data type: xlsx
Explanation note: Uncorrected *p*-distances between the *Odorrana* species based on the 16S gene sequences; * indicates that the samples are from Xiuwen, and # indicates that the samples are from Jinsha.
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Link: https://doi.org/10.3897/zse.101.161151.suppl2

Supplementary material 3

Supplementary table S3

Authors: Shize Li, Lang Mu, Jiahao Jing, Jing Liu, Yanlin Cheng, Bin Wang
Data type: xls
Explanation note: Uncorrected *p*-distances between the *Odorrana* species based on the COI gene sequences; * indicates that the samples are from Xiuwen, and # indicates that the samples are from Jinsha.
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Link: https://doi.org/10.3897/zse.101.161151.suppl3

Supplementary material 4

Supplementary figure S1

Authors: Shize Li, Lang Mu, Jiahao Jing, Jing Liu, Yanlin Cheng, Bin Wang

Data type: jpg

Explanation note: BI tree of the genus *Odorrana* was reconstructed based on the 16S gene sequences. Bayesian posterior probability/ML bootstrap supports were denoted beside each node, and "-" denotes BS < 50% or BPP < 0.60. Samples 1–89 refer to Table 1.

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Link: https://doi.org/10.3897/zse.101.161151.suppl4

Supplementary material 5

Supplementary figure S2

Authors: Shize Li, Lang Mu, Jiahao Jing, Jing Liu, Yanlin Cheng, Bin Wang

Data type: jpg

Explanation note: BI tree of the genus *Odorrana* was reconstructed based on the COI gene sequences. Bayesian posterior probability/ML bootstrap supports were denoted beside each node, and "-" denotes BS < 50% or BPP < 0.60. Samples 1–89 refer to Table 1.

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